
Title:, GROWTH ARREST HOMEOBOX GENE Inventors Name: Gorski, et al.; Serial No.: 09/940,673 Attorney Docket Number: 22311/04015

874 220	ACT	CTC L	GAC D	CTA	AAC I	6TG /	900 V	ATA (3AG /	AGA TAT GAG R Y E	AGA R	AGA R	CT6 L	AGA R) _	AAC TAT CTG A	TAT Y	AAC	CAT CAT	CAT H	9 9 9	TTC F	GAG GCA GAG TTC GCC E A E F A	GCA A	GAG
799	CTT	GAA E	AGA R	ATC I	CAA ATC Q I	GAG (AAA (ACC /	TTC /	GCT A	AÇ (-)	AGA R	GAA	AAG K	AGG R	CCT P	AAA K	AGC S	AAC	6T6 V	GAA E	TCA S	AAT TAC AAG TCA GAA N Y K S E	TAC Y	N N
724 176	66A 6	GAA	CAG Q	700 S	GAT 0	TCA (A61	GAC /	A60.	AAA	AGA R	AAA	\$ \(\text{\ti}\}\\ \text{\texi}\text{\text{\texi}\text{\text{\text{\text{\texi}\tint{\text{\ti}}\tint{\text{\texi}\tint{\text{\texitt{\text{\texi}\text{\texit{\t	9	AGT	AGA R	AAG K	GAG E	6T6 V	GAA E	GCA A	TCA CCC GCA		6CG CTG A L) A
649 151	CAA	CGT R	- 099 9	TAT ≺	. O	A6G (CCA /	9 P		909	- 225 •	gg.	ACC 1	විට අ	ACC 1	AGC S	700 S	9	CT6 L	A6C S	TCT TCT S S	TCT S	TGC TCC AAC 1 C S N	55 S	ပ္တ
574 126	CTC L	6TC V) P	CCT (A6C (AGC /	9	CTG (GAG () 900 6)) 		66A (70C N	GAT D	CCT P	CAG O	CTG L	76C C	CTT L	<u>کا</u> (ک	CGG CAC AGC R H S	000 R	6CG GCC A A	92 v
499	AGC S	CCA P) P	700 s	70C S	ATG 1	CAG A)))) DIO	CAC (, post	AAC N	AGC .	CAA	CTG	6CT A	CAG	CAC	CAG	CAG	CAG	CAG	CAC CAC CAG CAG	CAC T	용되
424	CAT H	E CAC	CAC (CAC (CAC (CAC (CAC	CAC C	CAC	999	A6G (R	CAC /	CAT (CAG 1	AGC (900 V	111 F	ATG M	ງ ວງງ	GAG E	GAG E	CCC AAT GAG P N E		GGA TAC G Y	SGA G
349	900 V	ATC 1	ATA I	76C / C	TCT 1	700 T	1001 S	101 I S	ACA 1	700 / S	CTC L	GAA (ر ا ا	TAC 1	₩ ₩	ATG M	CAC	GAC D	TCT S	AGA R	66A 6	CAT GGA H G	CTC L	CTG GCC L A). L
274 26	TCT S	TCT S	CAG	706 (S	11C 1	. 000 P	CAC 0	116 C	00C 1	CAA		ACA GCG T A	9 9 9	CAC () P	AGC) 29) 20)	CT6 L	ეე ე	9	Ë u	CTC _	GAA CAC CCC CTC TTT E H P L F	EAC H	JAA E
1	ATG M	ופככ	[GCA]	ACT	TGAG	AAGC	1166	CT6C	TCT	IGAAG	1706	SACC	r 166(3ACT.	6676	TAGTGAAAAGTGACAGCGCTTGGTGGACTTTGGGACCTTCGTGAAGTCTTCTGCTTGGAAGCTGAGACTTGCATGCC	CAGC	GTGA	AAA	AG TG	11101	166A1	GGGAGAGTCCTAGGATTTC	16A61	996
8	3166	3TGA(166A(ATT/	TIAC		9993	9000	CAAA	.1661	366.10	16CGC	3ATT/	3T66(AGGA	<u> AGGAGACTGGCCGCTCGGCTCAGGACTGGGATTAGCGGGCTCTGCTCAAACCCGGGGGTTTTACATTAGGAGTGAGT</u>	CTCG	9009	ACTG	166AG	166	TACC	GTCAAGTGTTTATACGTGC	AGTO	3TC/

949

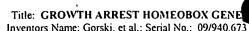
TTC CAG AAC AGG AGA ATG AAG TGG AAG

GAA AGA CAG GTG AAA GTG

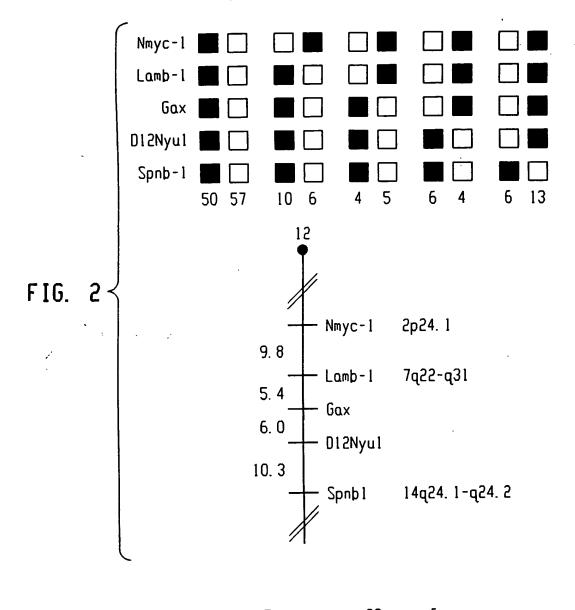
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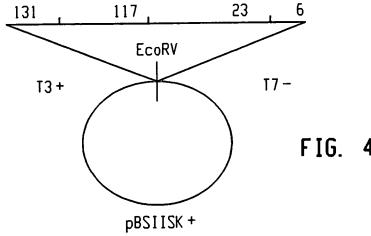
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1024 276	301	303	1296	1396	1496	1596	1696	1796	9681	9661	2096	2196	2244
GCA GCC CGA GAA AAG GAA CTG GTG AAA AAG GGA ACA CTT CTT CCA TCA GAG CTG TCA GGA ATT GGT GCA I A A A R E K E L V N V K K G $(\overline{\mathbf{T}})$ L L P S $\overline{\mathbf{E}}$ L S $\overline{\mathbf{G}}$ I $\overline{\mathbf{G}}$ A	GCC ACC CTC CAG CAG ACA GGG GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG CAC GCA I A T L Q Q T G D S L A N D D S R D S D H S S E H A	CAC ITA IGA TACATACAGAGACCAGCTCCGTTCTCAGGAAAGCACCATTGTGATGGCAAATCTCACCCAAACATCGTTTACATGGCAGATGACTGTG 1 H L STOP	GCAGTGTTGCTTAATATAAATTAAACGCAGGCATCTCAAGTCTGTTTCTCATGATTGAT	AGTGAAATTGGAGAAAGTGAACATATCTAAATATACTTGTTCCTTATATGACAGAGGGAGATGATGTTTGCTTTGCTTTGCCTTGCACTGAAAATTAAATTG	CTACCAAGAGCAAACTCGGTAAGACATITTGACTCAAGTTGTCTCCAGAGTGAAGATGTTATAGAAATGCTTTGAACATTCCAGTTGTACCAGGTCATGT	GTGTGACACTGGGCAGGTATTTGCTTTTGCTTGCACTGAAACTTAAACTGCTATCAAGTTAACCCATGAAATAGTTTATCTTGAACAGCCACAGTGCCTG	AAATCACCAAGTGGATATAAAATGAACTGAAATTCTGTATATTACTCCTAAGTCATTTTCCTGTCTTCACTAATTTTAGCAAATGCATTCATATTAGC	TGATGAAAATAGGCTTTCCCGTGGACAAATGCAGCCTCCTTGTATTTTTATACATTTTTTTGTCAGTCA	CAAGTAGAGGAAATGCAGTAGAGTCTGATAGGACATATTCTTGGTACCACAGACAAAACAAATCTTCTGTTGCATTGACTATCAACTGCTGCAGATACAT	TAGAGAACACACCTAGCCCCCCTCCTGTTATCGCTCGAAGACATTAGCGTCATAGGCAAGTAGTTACCTTGCCAAATGAGTCTTGTGTGG	CAGATGICTGATTITGTATCTTTAAACTGTTAATGGTATGTGTCTGCTTCAGTTAACAGGGAAAAAGATTTCTTCCTCATTGTTTATGATACAAAACCCA	AGTGCCAAACAAAGCTAGTTCTTCAAGGGATAGATGAGAAACTGAATGTCTGACAAGTAGACTCAGCGAAAATACATTATTTTCAGAGGCTGTGTATTC	A TGCAGTACAAGTCCTTGTATTTTGTAAAAAAAAAAAAA



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21.7 21.7 758 242 833 267 267 908 292 302 6666 6666 6666 6666 6666 6666 6666 6666 CAG ACC GGA GGA CTG CTG CTG GGA GGA GGA GGA SCC AACC AACC AACC TA A A A AAC > 216 > A D A N TAT Y CAT AAT H N A6C S GTC AAC / 6A6 E STCTTCTACCTGGAACCCGAAACTTGCATGCT ATG GAA CAC CCG CTC TTT
M E H P L F GAA E CAG EAT H TAC CCC AAC G
CAT CAG CAG C
H Q Q
CGG CAT AGC C
R H S
AAC TCT TCC A
N S S
TCA CCT GCG C
S P A
AAG TCA GAA C
K S E 9 9 ۲ CAG 0 0 CGG R R SCC (A GAA E 36A GCA AGA R GCT ACC C1C AAT N GAA GAA E E E A A TGC C S S A T A 55 S AAA K GCA AAG K K GAG

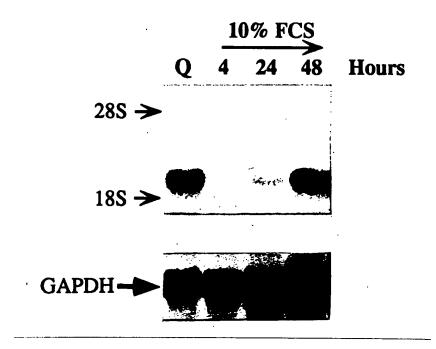


FIG. 5A

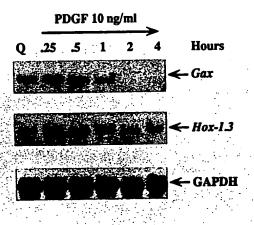
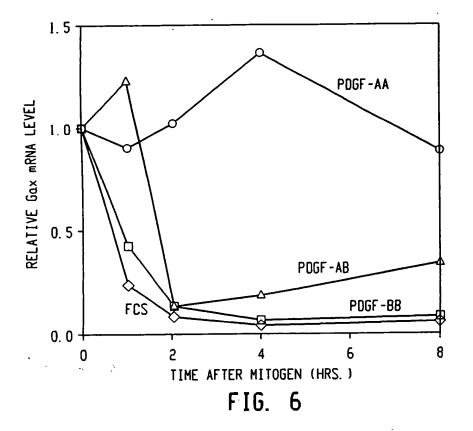
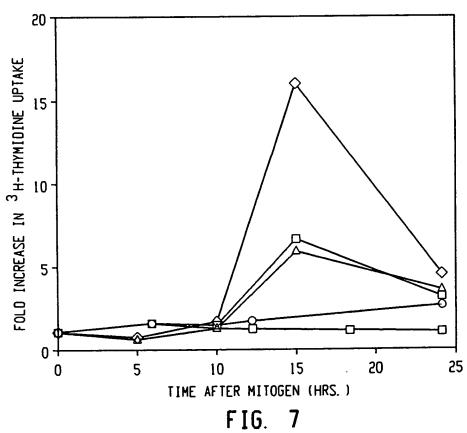


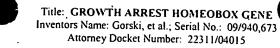
FIG. 5B

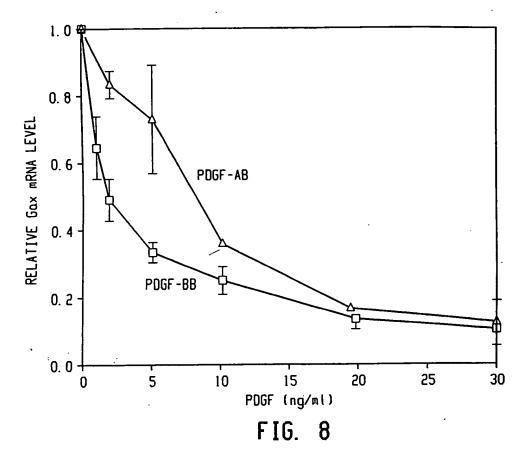
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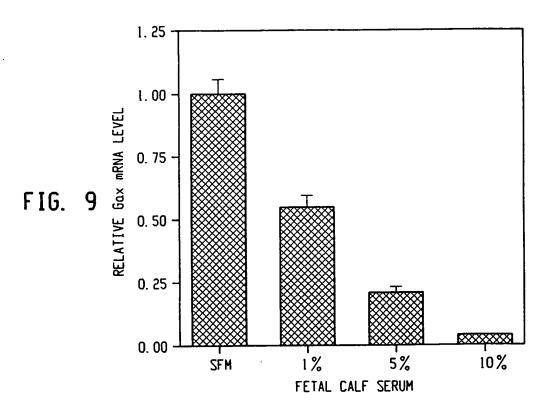
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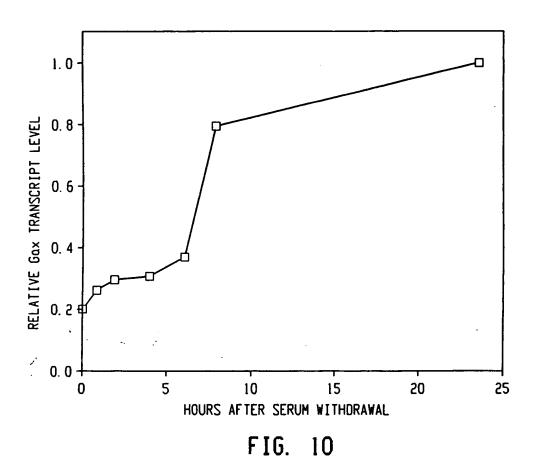


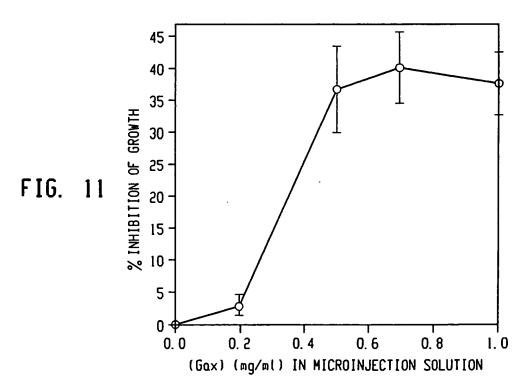












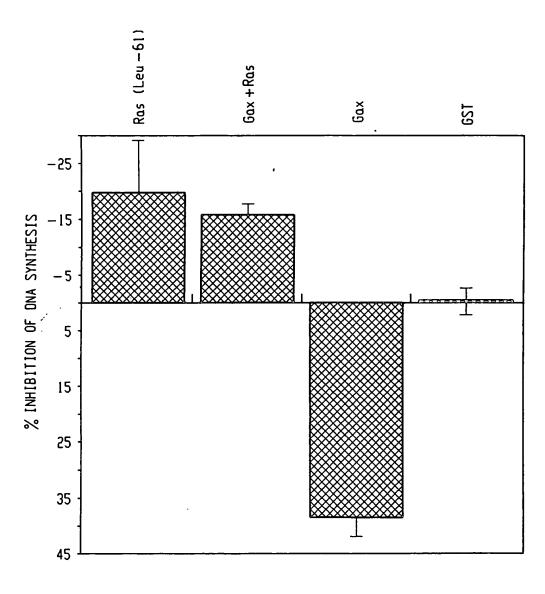
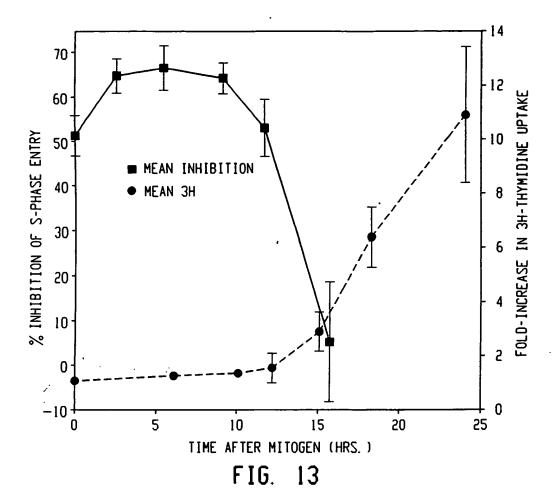


FIG. 12



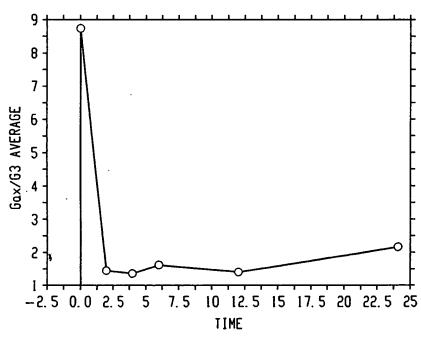


FIG. 14

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